

REMARKS

Status of the Claims

Claim 1 has been amended without prejudice to or disclaimer of the subject matter therein such that it now recites the following: "An isolated nucleic acid comprising a polynucleotide having at least 80% sequence identity to SEQ ID NO: 3, wherein said polynucleotide encodes a maize AFP1 protein, or a complement of said polynucleotide." Support for this amendment is found in original claim 1. New claims 13-17 have been added, drawn to the polynucleotide sequences of SEQ ID NOS:1, 3, 5, 7 and 9. Support for the new claims can be found in original claim 1. Therefore, no new matter has been added by amendment. Claims 1-17 are now pending.

With respect to Item 1 on the Office Action Summary, the Examiner has indicated that the Restriction Requirement is responsive to the Communication filed on February 5, 2003. Applicants wish to clarify that the Communication filed on February 5, 2003 was a Request for Corrected Filing Receipt.

It is not believed that extensions of time or fees for net addition of claims are required, beyond those that may otherwise be provided for in documents accompanying this paper. However, in the event that additional extensions of time are necessary to allow consideration of this paper, such extensions are hereby petitioned under 37 CFR § 1.136(a), and any fee required therefore (including fees for net addition of claims) is hereby authorized to be charged to Deposit Account No. 16-0605.

Respectfully submitted,



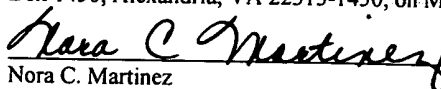
Eric J. Kron

Registration No. 45,941

Customer No. 00826
ALSTON & BIRD LLP
Bank of America Plaza
101 South Tryon Street, Suite 4000
Charlotte, NC 28280-4000
Tel Raleigh Office (919) 862-2200
Fax Raleigh Office (919) 862-2260

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, on May 22, 2003.


Nora C. Martinez

Alignment of the Maize sequences:

```

      1                               50
SEQ ID: 1 (1) ---ACCCACGCGTCCGCCACGCGTCCGC--AGCAATCCACACAAGCACT
SEQ ID: 3 (1) ---ACCCACGCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
SEQ ID: 5 (1) TCGACCCACGCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
SEQ ID: 7 (1) TCGACCCACGCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
SEQ ID: 9 (1) -----AGCG
Consensus (1) ACCCACGCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      51                               100
1 (46) TCGAAGGACCACTG-CTCGGAG---GACACACCAAGCGTCTGCACCAAT
3 (48) TCGACGTACACGGGCGCTGCGCACAGACACACCAAGCGTCCGGCACCAT
5 (51) TCGACGTACACGGGCGCTGCGCACAGACACACCAAGCGTCCGGCACCAT
7 (51) TCGACGTACACGGGCGCTGCGCACAGACACACCAAGCGTCCGGCACCAT
9 (5) GCGGGGAAGAAGCGCTACAAGATGAAGACGACAGGCGTCCGGCACCAT
Consensus (51) TCGACGTC CACGGGCGCTGCGCACAGACACACCAAGCGTCCGGCACCAT
      101                               150
1 (91) GGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCCGTGG
3 (98) GGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCCGTGG
5 (101) GGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCCGTGG
7 (101) GGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCCGTGG
9 (55) GGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCCGTGG
Consensus (101) GGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCCGTGG
      151                               200
1 (141) CCCC GGCCGGCTTCGGCCGCCACGGCGGCGGCTCCAGCAGCACGTCGTC
3 (148) CCCC GGCCGGCTTCGGCCGCCACGGCGGCGGCTCCAGCAGCACGTCGTC
5 (151) CCCC GGCCGGCTTCGGCCGCCACGGCGGCGGCTCCAGCAGCACGTCGTC
7 (151) CCCC GGCCGGCTTCGGCCGCCACGGCGGCGGCTCCAGCAGCACGTCGTC
9 (105) CCCC GGCCGGCTTCGGCCGCCACGGCGGCGGCTCCAGCAGCACGTCGTC
Consensus (151) CCCC GGCCGGCTTCGGCCGCCACGGCGGCGGCTCCAGCAGCACGTCGTC
      201                               250
1 (191) AAGGAGAAGTTCGAGGAGGTGACACGGTATCACGCGCCGGCGCCAAACCA
3 (198) AAGGAGAAGTTCGAGGAGGTGACACGGTATCACGCGCCGGCGCCAAACCA
5 (201) AAGGAGAAGTTCGAGGAGGTGACACGGTATCACGCGCCGGCGCCAAACCA
7 (201) AAGGAGAAGTTCGAGGAGGTGACACGGTATCACGCGCCGGCGCCAAACCA
9 (155) AAGGAGAAGTTCGAGGAGGTGACACGGTATCACGCGCCGGCGCCAAACCA
Consensus (201) AAGGAGAAGTTCGAGGAGGTGACACGGTATCACGCGCCGGCGCCAAACCA
      251                               300
1 (241) CCACCACCACCA---TGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCG
3 (248) CCACCACCACCA---TGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCG
5 (251) CCACCACCACCA---TGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCG
7 (251) CCACCACCACCAATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCG
9 (205) CCACCACCACCA---TGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCG
Consensus (251) CCACCACCACCA TGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCG
      301                               350
1 (288) AGACCAGGGTCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAG
3 (295) AGACCAGGGTCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAG
5 (298) AGACCAGGGTCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAG
7 (301) AGACCAGGGTCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAG
9 (252) AGACCAGGGTCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAG
Consensus (301) AGACCAGGGTCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAG
      351                               400
1 (338) CGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCCGG- CGGCCGG
3 (345) CGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCCGG- CGGCCGG
5 (348) CGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCCGG- CGGCCGG
7 (351) CGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCCGG- CGGCCGG
9 (302) CGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCA GCCCGG CGGCCGG
Consensus (351) CGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCCGG CGGCCGG
      401                               450
1 (387) CATCCACGCCCCTTCGTGCTTGCTGCGTGCTTATGTATGTCTGTGGTT
3 (394) CATCCACGCCCCTTCGTGCTTGCTGCGTGCTTATGTATGTCTGTGGTT
5 (397) CATCCACGCCCCTTCGTGCTTGCTGCGTGCTTATGTATGTCTGTGGTT
7 (400) CATCCACGCCCCTTCGTGCTTGCTGCGTGCTTATGTATGTCTGTGGTT
9 (352) CATCCACGCCCCTTCGTGCTTGCTGCGTGCTTATGTATGTCTGTGATT
Consensus (401) CATCCACGCCCCTTCGTGCTTGCTGCGTGCTTATGTATGTCTGTGGTT
      451                               500
1 (437) GACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTC
3 (444) GACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTC
5 (447) GACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTC
7 (450) GACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTC

```

```

9 (402) G--TG-----CAGGGTCATCGTACTTGGCTAGCGTACGTGCACGCACTC
Consensus (451) GACTGGTTGT CAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTC
501 550
1 (487) AGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCT
3 (494) AGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCT
5 (497) AGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCT
7 (500) AGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCT
9 (444) AGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCT
Consensus (501) AGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCT
551 600
1 (537) TCGTAATACTAAATACCTACATCAAAAAAAAAAAAAAAAAAAAAAAAAA
3 (544) TCGTAATACTAA-----AAAAAAAAAAAAAAAAAAAAAAAAA
5 (547) TCGTAATACTAA-----AAAAAAAAAAAAAAAAAAAAAAAAA
7 (550) TCGTAATACTAA-----AAAAAAAAAAAAAAAAAAAAAAAAA
9 (494) TCGTAATACTAAATACCT-----AAAAAAAAAAAAAAAAAAAAAAAAA
Consensus (551) TCGTAATACTAA AAAAAAAAAAAAAAAAAAAAAAAAAA
601 650
1 (587) AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
3 (575) -----
5 (578) -----
7 (581) -----
9 (530) -----
Consensus (601) -----
651 690
1 (637) AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
3 (575) -----
5 (578) -----
7 (581) -----
9 (530) -----
Consensus (651) -----

```



Maize Sequences: Gap-like results with Needleman-Wunsch algorithm

Seq1	Seq2	Overall id
3	1	82.1
3	5	99.48
3	7	86.76
3	9	86.76

Sequence #3's identity to the other sequences is shown above.

Pairwise Alignments of Sequence 3 versus each of the other maize sequences.
(Gap-like results with Needleman-Wunsch algorithm "Needle program")

GLOBAL: 3 VS 1
SCORE: 2683.50

3	1	ACCCACGCGTCCGCCCACGCGTCCGCACAGCAATCCACACAAGCA 45
1	1	ACCCACGCGTCCGCCCACGCGTCCG . CAGCAATCCACACAAGCA 43
3	46	CTTCGACGTCAACGGGCGCTGCGCACA . GACACACCAAGCGTCG 89
1	44	CTTCGA AGGACCACTGCTCGGAGGACACACCAAGCGTCT 82
3	90	GCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAG 134
1	83	GCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAG 127
3	135	GTGAGGTCGGTGGCCCGGCCGGCTTCGGCCGCCACGGCGGCGGC 179
1	128	GTGAGGTCGGTGGCCCGGCCGGCTTCGGCCGCCACGGCGGCGGC 172
3	180	GTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACG 224
1	173	GTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACG 217
3	225	GTCTCAGCGCCGGCGCCAACCACCACCACCACCATGGTCACCAC 269
1	218	GTATCAGCGCCGGCGCCAACCACCACCACCACCATGGTCACCAC 262
3	270	GGCGGCCACGGCTTCGTGGTGC GCGAGACCAGGGTCGAAGAGGAC 314
1	263	GGCGGCCACGGCTTCGTGGTGC GCGAGACCAGGGTCGAGGAGGAC 307
3	315	ATCAACACCTGCACCGCGAGGTCCACGAGCGCAGGGAGAGCTTC 359
1	308	ATCAACACCTGCACCGCGAGGTCCACGAGCGCAGGGAGAGCTTC 352
3	360	CTCGCCAGGGCTAACTGAGCCGCCCGGCGGCCGGCATCCACGCC 404
1	353	CTCGCCAGGGCTAACTGAGCCGCCCGGCGGCCGGCATCCACGCC 397
3	405	GTTCTGTCTTGCCTGCGTGCCTTATGTATGTCTGTGGTTGACTGG 449
1	398	GTTCTGTCTTGCCTGCGTGCCTTATGTATGTCTGTGGTTGACTGG 442
3	450	TTGTTTCAAGGTCATCGTACTTGGCTATCGTACGTGCACGCACTCA 494
1	443	TTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTCA 487
3	495	GCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAAC 539
1	488	GCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAAC 532
3	540	TTCTTCGTAATACTAA AAAAAAAAAAAAAAAAAAAAA 574
1	533	TTCTTCGTAATACTAATACTACATCAAAAAAAAAAAAAAAAAAAAA 577
3		
1	578	AA 622

3

1

623

AA 667

3

1

668

AAAAAAAAAA

676

OVERALL %ID = 82.10

OVERALL %SIMILARITY = 82.10

GLOBAL: 3 VS 5
SCORE: 2870.00

3	1	ACCCACGCGTCCGCCCACGCGTCCGCACAGCAATCCACACAA	42
5	1	TCGACCCACGCGTCCGCCCACGCGTCCGCACAGCAATCCACACAA	45
3	43	GCACTTCGACGTCACACGGGCGCTGCGCACAGACACACCAAGCGT	87
5	46	GCACTTCGACGTCACACGGGCGCTGCGCACAGACACACCAAGCGT	90
3	88	CGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGG	132
5	91	CGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGG	135
3	133	AGGTGAGGTCGGTGGCCCCGGCCGGCTTCGGCCGCCACGGCGGCG	177
5	136	AGGTGAGGTCGGTGGCCCCGGCCGGCTTCGGCCGCCACGGCGGCG	180
3	178	GCGTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACA	222
5	181	GCGTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACA	225
3	223	CGGTCTCAGCGCCGGCGCCAACCACCACCACCACCATGGTCACC	267
5	226	CGGTCTCAGCGCCGGCGCCAACCACCACCACCACCATGGTCACC	270
3	268	ACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGG	312
5	271	ACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGG	315
3	313	ACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCT	357
5	316	ACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCT	360
3	358	TCCTCGCCAGGGCTAACTGAGCCGCCCGGCGGCCGGCATCCACGC	402
5	361	TCCTCGCCAGGGCTAACTGAGCCGCCCGGCGGCCGGCATCCACGC	405
3	403	CCGTTTCGTGCTTGCCTGCGTGCCTTATGTATGTCTGTGGTTGACT	447
5	406	CCGTTTCGTGCTTGCCTGCGTGCCTTATGTATGTCTGTGGTTGACT	450
3	448	GGTTGTTTCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACT	492
5	451	GGTTGTTTCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACT	495
3	493	CAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAA	537
5	496	CAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAA	540
3	538	ACTTCTTCGTAATACTAAAAAAAAAAAAAAAAAAAAA	574
5	541	ACTTCTTCGTAATACTAAAAAAAAAAAAAAAAAAAAA	577

OVERALL %ID = 99.48

OVERALL %SIMILARITY = 99.48

GLOBAL: 3 VS 7
SCORE: 2336.50

3	1	ACCCACGCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCA	45
7	1	AG..	2
3	46	CTTCGAC..GTCACACGGG.....GCTGCGCACAGACACACCAA	83
7	3	...CGGCGGGGAAGAAGGGCTACAAGATG....AAGACGCACAAG	40
3	84	GCGTCGGCACC AATGGCTTACTACCAGGAGGTGGACTACTGCTCG	128
7	41	GCGTCGGCACC AATGGCTTACTACCAGGAGGTGGACTACTGCTCG	85
3	129	GAGGAGGTGAGGTGCGGTGGCCCCGGCCGGCTTCGGCCGCCACGGC	173
7	86	GAGGAGGTGAGGTGCGGTGGCCCCGGCCGGCTTCGGCCGCCACGGC	130
3	174	GGCGGCGTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTC	218
7	131	GGCGGCGTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTC	175
3	219	GACACGGTCTCACGCGCCGGCGCCAACCACCACCACCACCATGGT	263
7	176	GACACGGTCTCACGCGCCGGCGCCAACCACCACCACCACCATGGT	220
3	264	CACCACGGCGGCCACGGCTTCGTGGTGCGGAGACCAGGGTCGAA	308
7	221	CACCACGGCGGCCACGGCTTCGTGGTGCGGAGACCAGGGTCGAG	265
3	309	GAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAG	353
7	266	GAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAG	310
3	354	AGCTTCCTCGCCAGGGCTAACTGAGCCGCCC.GGCGGCCGGCATC	397
7	311	AGCTTCCTCGCCAGGGCTAACTGAGCAGCCGGGCGGCCGGCATC	355
3	398	CACGCCCGTTTCGTGCTTGCCTGCGTGCCTTATGTATGTCTGTGGT	442
7	356	CACGCCCGTTTCGTGCTTGCCTGCGTGCCTTATGTATGTCTG....	396
3	443	TGACTGGTTGTTTCAGGGTCATCGTACTTGGCTATCGTACGTGCAC	487
7	397TGATTGTGCAGGGTCATCGTACTTGGCTAGCGTACGTGCAC	437
3	488	GCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGA	532
7	438	GCACTCAGCTCCTGTACGAATTACGATAATAAGCTCGTGACCTGA	482
3	533	ATAAACTTCTTCGTAATACTAA.....AAAAAAAAAAAAAAAAA	572
7	483	ATAAACTTCTTCGTAATACTAATACTTAAAAAAAAAAAAAAAAA	527
3	573	AA	574
7	528	AA	529

OVERALL %ID = 86.76

OVERALL %SIMILARITY = 86.76

GLOBAL: 3 VS 9
SCORE: 2336.50

3	1	ACCCACGCGTCCGCCCACGCGTCCGCACAGCAATCCACACAAGCA	45
9	1		AG.. 2
3	46	CTTCGAC..GTCACACGGGC.....GCTGCGCACAGACACACCAA	83
9	3	...CGGCGGGGAAGAAGGGCTACAAGATG...AAGACGCACAAG	40
3	84	GCGTCGGCACC AATGGCTTACTACCAGGAGGTGGACTACTGCTCG	128
9	41	GCGTCGGCACC AATGGCTTACTACCAGGAGGTGGACTACTGCTCG	85
3	129	GAGGAGGTGAGGTGCGTGGCCCCGGCCGGCTTCGGCCGCCACGGC	173
9	86	GAGGAGGTGAGGTGCGTGGCCCCGGCCGGCTTCGGCCGCCACGGC	130
3	174	GGCGGCGTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTC	218
9	131	GGCGGCGTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTC	175
3	219	GACACGGTCTCACGCGCCGGCGCCAACCACCACCACCACCATGGT	263
9	176	GACACGGTCGCACGCGCCGGCGCCAACCACCACCACCACCATGGT	220
3	264	CACCACGGCGGCCACGGCTTCGTGGTGCGGAGACCAGGGTCGAA	308
9	221	CACCACGGCGGCCACGGCTTCGTGGTGCGGAGACCAGGGTCGAG	265
3	309	GAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAG	353
9	266	GAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAG	310
3	354	AGCTTCCTCGCCAGGGCTAACTGAGCCGCCC.GGCGGCCGGCATC	397
9	311	AGCTTCCTCGCCAGGGCTAACTGAGCAGCCGGGCGGCCGGCATC	355
3	398	CACGCCCGTTTCGTGCTTGCCTGCGTGCCTTATGTATGTCTGTGGT	442
9	356	CACGCCCGTTTCGTGCTTGCCTGCGTGCCTTATGTATGTCTG... 396	
3	443	TGACTGGTTGTTTCAGGGTCATCGTACTTGGCTATCGTACGTGCAC	487
9	397	...TGATTGTGCAGGGTCATCGTACTTGGCTAGCGTACGTGCAC	437
3	488	GCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGA	532
9	438	GCACTCAGCTCCTGTACGAATTACGATAATAAGCTCGTGACCTGA	482
3	533	ATAAACTTCTTCGTAATACTAA...AAAAAAAAAAAAAAAAAAAA	572
9	483	ATAAACTTCTTCGTAATACTAATAACCTAAAAAAAAAAAAAAAAAAAA	527
3	573	AA	574
9	528	AA	529

OVERALL %ID = 86.76

OVERALL %SIMILARITY = 86.76